

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:36:02 ; Search time 15.7956 Seconds  
(without alignments)  
982.052 Million cell updates/sec

Title: US-09-625-573-2  
Perfect score: 1970  
Sequence: 1 MLSTSRFRINTNESGEV.....GKGKSIGRAPEASLQDKEGA 374

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1970	100.0	374	1	CKR2_HUMAN
2	1614.5	82.0	360	1	CKR2_MACMU
3	1346.5	68.4	373	1	CKR2_RAT
4	1332.5	67.6	373	1	CKR2_MOUSE
5	1244	63.1	354	1	CKR5_MOUSE
6	1236	62.7	352	1	CKR5_CERTO
7	1236	62.7	352	1	CKR5_HYLLE
8	1230	62.4	352	1	CKR5_MACMU
9	1230	62.4	352	1	CKR5_PANTR
10	1230	62.4	352	1	CKR5_PONPY
11	1230	62.4	354	1	CKR5_RAT
12	1228	62.3	352	1	CKR5_GORGO
13	1228	62.3	352	1	CKR5_PAPHA
14	1224	62.1	352	1	CKR5_HUMAN
15	1224	62.1	352	1	CKR5_PYGNE
16	1223	62.1	352	1	CKR5_PYGBI
17	1223	62.1	352	1	CKR5_TRAFR
18	1223	62.1	352	1	CKR5_TAPH
19	1211	61.5	352	1	CKR5_CERAE
20	967.5	49.1	355	1	CKR1_HUMAN
21	951.5	48.3	359	1	CKR3_MOUSE
22	945	48.0	359	1	CKR3_RAT
23	931.5	47.3	358	1	CKR3_CAVPO
24	911.5	46.3	355	1	CKR1_MACMU
25	899.5	45.7	355	1	CKR1_MOUSE
26	886.5	45.0	355	1	CKR3_HUMAN
27	876	44.5	355	1	CKR3_MACMU
28	867	44.0	355	1	CKR3_CERAE
29	833	42.3	360	1	CKR4_MOUSE
30	831.5	42.2	360	1	CKR4_HUMAN
31	731	37.1	356	1	CKRV_MOUSE
32	723	36.7	355	1	CKR8_HUMAN
33	716.5	36.4	356	1	CKR8_MACMU

34	708.5	36.0	353	1	CKR8_MOUSE
35	704.5	35.8	354	1	C3X1_RAT
36	698	35.4	355	1	C3X1_HUMAN
37	692	35.1	354	1	C3X1_MOUSE
38	588	29.8	384	1	CKD6_HUMAN
39	584	29.6	378	1	CKR7_HUMAN
40	580	29.4	378	1	CKD6_MOUSE
41	575.5	29.2	378	1	CKR7_MOUSE
42	575	29.2	382	1	CKD6_RAT
43	569	28.9	357	1	CKR9_HUMAN
44	564	28.6	367	1	CKR6_MOUSE
45	563	28.6	369	1	CKR9_MOUSE

ALIGNMENTS

RESULT 1  
CKR2\_HUMAN  
ID CKR2\_HUMAN STANDARD; PRT; 374 AA.  
AC P41597;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 2 (C-CR2) (CCR-2) (CCR2)  
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CCR2).  
GN CCR2 OR CMKR2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94195821; PubMed=8146186;  
RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,  
RA Coughlin S.R.;  
RA "Molecular cloning and functional expression of two monocyte  
RT chemoattractant protein 1 receptors reveals alternative splicing of  
RT the carboxyl-terminal tails";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94324942; PubMed=8048929;  
RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;  
RT "cDNA cloning and functional expression of a human monocyte  
RT chemoattractant protein 1 receptor";  
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97150864; PubMed=8995400;  
RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;  
RT "Organization and differential expression of the human monocyte  
RT chemoattractant protein 1 receptor gene. Evidence for the role of the  
RT carboxyl-terminal tail in receptor trafficking";  
RL J. Biol. Chem. 272:1038-1045(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,  
RA Nham M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,  
RA Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J.,  
RA Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M.,  
RA Porcel B.M., Dragan Y., Glacalone J., Pae A., Powell E.,  
RA Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y.,  
RA Watanabe M., Doggett N., Garcia D., Sagripanti J.I.;  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SULFATION OF TYR-26, AND N-GLYCOSYLATION.  
RX MEDLINE=20501139; PubMed=11046064;  
RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,  
RA Chakravarty L., Kolattukudy P.E.;  
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that  
RT has tyrosine sulfation in a conserved extracellular N-terminal  
RT region.";

J. Immunol. 165:5295-5303(2000).

CC -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 CC Transduces a signal by increasing the intracellular calcium ions  
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- PTM: N-GLYCOSYLATED.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: U03882; AAA19119.1; -  
 CC EMBL: U03905; AAA19120.1; -  
 CC EMBL: D29984; BAA06253.1; -  
 CC EMBL: U80924; AAC51637.1; -  
 CC EMBL: U80924; AAC51636.1; -  
 CC EMBL: U95626; AAB57791.1; -  
 CC EMBL: U95626; AAB57792.1; -  
 CC Genbank: HGNC:1603; CCR2.  
 CC MIM: 601267; -  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7tm.1; 1.  
 CC PRINTS: PR00237; GPCR\_RHODOPSIN.  
 CC PROSITE: PS00237; G-PROTEIN\_RECEP\_FL1; 1.  
 CC PROSITE: PS00262; G-PROTEIN\_RECEP\_FL2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 CC Alternative splicing.  
 CC DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 43 70 1 (POTENTIAL).  
 CC DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 81 100 2 (POTENTIAL).  
 CC DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 115 136 3 (POTENTIAL).  
 CC DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 154 178 4 (POTENTIAL).  
 CC DOMAIN 179 206 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 207 226 5 (POTENTIAL).  
 CC DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 244 268 6 (POTENTIAL).  
 CC DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 286 309 7 (POTENTIAL).  
 CC DOMAIN 310 374 CYTOPLASMIC (POTENTIAL).  
 CC CARBOHYD 14 14 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC MOD\_RES 26 26 SULFATION.  
 CC DISULFD 113 190 BY SIMILARITY.  
 CC VARSPLIC 314 374 SLFIALGCRAPLQKPVCGGVRPKNVKVTQGLDGR  
 CC GKSGSTIGRAPEASLDQKEGA -> RYLSVFFRRKHTRCK  
 CC QCPVYRETVDCVSTSTPTSGEQEVSAGL (IN  
 CC ISOFORM B).  
 CC  
 CC SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;  
 CC  
 CC Query Match 100.0%; Score 1970; DB 1; Length 374;  
 CC Best Local Similarity 100.0%; Pred. No. 3.7e-115;  
 CC Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKEDVDKQIGAOQLLPPLYSLVFIFGVGN 60  
 CC |  
 CC 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKEDVDKQIGAOQLLPPLYSLVFIFGVGN 60  
 CC |  
 CC 61 MLVVLINCKKLCITDIYLNLAISDLFLITPLWAHSAANWVFGNAMCKLFTGLY 120  
 CC |  
 CC 61 MLVVLINCKKLCITDIYLNLAISDLFLITPLWAHSAANWVFGNAMCKLFTGLY 120  
 CC |  
 CC 121 HIGYGGGFFIILLTIDRYLATVHAFAKARTVFGVVTSVITWLVAVFASVPGIIFTK 180  
 CC |  
 CC 121 HIGYGGGFFIILLTIDRYLATVHAFAKARTVFGVVTSVITWLVAVFASVPGIIFTK 180  
 CC |

QY 181 CQKEDSVYVCGPFPGRWNNFHTIMRNILGLVLPLLMVICYSGLTKTLRCRNEKKRHR 240  
 |  
 Db 181 CQKEDSVYVCGPFPGRWNNFHTIMRNILGLVLPLLMVICYSGLTKTLRCRNEKKRHR 240  
 |  
 QY 241 AVRVIETIMVYELFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLGTHCCI 300  
 |  
 Db 241 AVRVIETIMVYELFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLGTHCCI 300  
 |  
 QY 301 NPIIYAFVGEKFSRLFHIALGCRAPLQKPVCGGVRPKNVKVTQGLDGRGKSKI 360  
 |  
 Db 301 NPIIYAFVGEKFSRLFHIALGCRAPLQKPVCGGVRPKNVKVTQGLDGRGKSKI 360  
 |  
 QY 361 GRAPEASLDQKEGA 374  
 |  
 Db 361 GRAPEASLDQKEGA 374  
 |  
 RESULT 2  
 CCR2\_MACMU  
 ID CCR2\_MACMU STANDARD; PRT; 360 AA.  
 AC O18793;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-C CCR-2) (CC-CCR-2) (CCR-2) (CCR2)  
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CCR2).  
 GN CCR2 OR CCR2.  
 OS Macaca mulatta (Rhesus macaque).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 CC Cercopithecinae; Macaca.  
 CC NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21354176; PubMed=11461684;  
 RA Margulies B.J., Hauer D.A., Clements J.E.;  
 RT "Identification and comparison of eleven rhesus macaque chemokine  
 RT receptors.";  
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
 CC -1- FUNCTION: RECEPTOR FOR THE MCP-1, MCP-3 AND MCP-4 CHEMOKINES.  
 CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS  
 CC LEVEL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC  
 CC EMBL: AF013958; AAD11572.1; -  
 CC InterPro: IPR000276; GPCR\_Rhodopsn.  
 CC Pfam: PF00001; 7tm.1; 1.  
 CC PRINTS: PR00237; GPCR\_RHODOPSIN.  
 CC PROSITE: PS00237; G-PROTEIN\_RECEP\_FL1; 1.  
 CC PROSITE: PS00262; G-PROTEIN\_RECEP\_FL2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 CC Alternative splicing.  
 CC DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 43 70 1 (POTENTIAL).  
 CC DOMAIN 71 80 2 (POTENTIAL).  
 CC TRANSMEM 81 100 3 (POTENTIAL).  
 CC DOMAIN 101 114 4 (POTENTIAL).  
 CC TRANSMEM 115 136 5 (POTENTIAL).  
 CC DOMAIN 137 153 6 (POTENTIAL).  
 CC TRANSMEM 154 178 7 (POTENTIAL).  
 CC DOMAIN 179 206 8 (POTENTIAL).  
 CC TRANSMEM 207 226 9 (POTENTIAL).  
 CC DOMAIN 227 243 10 (POTENTIAL).  
 CC TRANSMEM 244 268 11 (POTENTIAL).  
 CC DOMAIN 269 285 12 (POTENTIAL).  
 CC TRANSMEM 286 309 13 (POTENTIAL).  
 CC DOMAIN 310 374 14 (POTENTIAL).  
 CC CARBOHYD 14 14 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC MOD\_RES 26 26 SULFATION.  
 CC DISULFD 113 190 BY SIMILARITY.  
 CC VARSPLIC 314 374 SLFIALGCRAPLQKPVCGGVRPKNVKVTQGLDGR  
 CC GKSGSTIGRAPEASLDQKEGA -> RYLSVFFRRKHTRCK  
 CC QCPVYRETVDCVSTSTPTSGEQEVSAGL (IN  
 CC ISOFORM B).  
 CC  
 CC SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;  
 CC  
 CC Query Match 100.0%; Score 1970; DB 1; Length 374;  
 CC Best Local Similarity 100.0%; Pred. No. 3.7e-115;  
 CC Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 CC 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKEDVDKQIGAOQLLPPLYSLVFIFGVGN 60  
 CC |  
 CC 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKEDVDKQIGAOQLLPPLYSLVFIFGVGN 60  
 CC |  
 CC 61 MLVVLINCKKLCITDIYLNLAISDLFLITPLWAHSAANWVFGNAMCKLFTGLY 120  
 CC |  
 CC 61 MLVVLINCKKLCITDIYLNLAISDLFLITPLWAHSAANWVFGNAMCKLFTGLY 120  
 CC |  
 CC 121 HIGYGGGFFIILLTIDRYLATVHAFAKARTVFGVVTSVITWLVAVFASVPGIIFTK 180  
 CC |  
 CC 121 HIGYGGGFFIILLTIDRYLATVHAFAKARTVFGVVTSVITWLVAVFASVPGIIFTK 180  
 CC |

FT TRANSMEM 207 226 5 (POTENTIAL).  
 FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 244 268 6 (POTENTIAL).  
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 286 309 7 (POTENTIAL).  
 FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 14 14 N-LINKED (GLCNAC... (POTENTIAL).  
 FT MOD\_RES 26 26 SULFATION (BY SIMILARITY).  
 FT DISULFID 113 190 BY SIMILARITY.  
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;  
 Query Match 82.0%; Score 1614.5; DB 1; Length 360;  
 Best Local Similarity 96.6%; Pred. No. 3.1e-93;  
 Matches 308; Conservative 4; Mismatches 4; Indels 3; Gaps 1;  
 QY 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHFDVKGQGAQLPPLSLVIFGFVGN 60  
 DB 1 MLSTSRFRIRNTNGSEVTTFFDYDGAPCHFDVKGQGAQLPPLSLVIFGFVGN 60  
 QY 61 MLVLLINCKKLCITDIYLLNLAISDLFLITPLMAHSAANEWVFGNCKLFTGLY 120  
 DB 61 MLVLLINCKKLCITDIYLLNLAISDLFLITPLMAHSAANEWVFGNCKLFTGLY 120  
 QY 121 HIGYFGGIFILLTIDRYLAIVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 DB 121 HIGYFGGIFILLTIDRYLAIVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 QY 181 CQEDSVYVCGPYFPRGNWFFHTMRNLTGLVLLIMVICYSGILTKLLRCNEKKRHR 240  
 DB 181 CQEDSVYVCGPYFPRGNWFFHTMRNLTGLVLLIMVICYSGILTKLLRCNEKKRHR 240  
 QY 241 AVRFTIMIVYFLFWTPYVNIIVLLNTFQEFGLSNCESTSQDQATQVTTGLMTHCCI 300  
 DB 241 AVRFTIMIVYFLFWTPYVNIIVLLNTFQEFGLSNCESTSQDQATQVTTGLMTHCCI 300  
 QY 301 NPIIYAFVGEKFR---SLF 316  
 DB 301 NPIIYAFVGEKFRRLSMF 319  
 RESULT 3  
 CKR2\_RAT STANDARD; PRT; 373 AA.  
 AC O55193;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2).  
 EN Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=98318173; PubMed=9655467;  
 RA Jiang Y., Salafian M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 RA defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 RT "Chemokine receptor expression in cultured glia and rat experimental  
 RT allergic encephalomyelitis.";  
 RL J. Neuroimmunol. 86:1-12(1998).  
 CC -!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5  
 CC CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR  
 CC CALCIUM IONS LEVEL (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND  
 CC MACROPHAGES.  
 CC -!- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC  
 CC ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 CC EMBL: U77349; AAC03242.1;  
 CC InterPro: IPR000276; GPCR\_Rhodpsn.  
 CC Pfam: PF00001; 7tm1; 1.  
 CC PRINTS: PR00237; GPCRHHODPSN.  
 CC PROSITE: PS00237; G-PROTEIN\_RECEPT\_F1\_1; 1.  
 CC PROSITE: PS0262; G-PROTEIN\_RECEPT\_F1\_2; 1.  
 CC G-protein coupled receptor; Transmembrane.  
 CC DOMAIN 1 60  
 CC EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 61 81  
 CC DOMAIN 82 91  
 CC POTENTIAL.  
 CC TRANSMEM 92 112  
 CC POTENTIAL.  
 CC DOMAIN 113 128  
 CC EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 129 149  
 CC POTENTIAL.  
 CC DOMAIN 150 170  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 171 191  
 CC POTENTIAL.  
 CC DOMAIN 192 220  
 CC EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 221 241  
 CC POTENTIAL.  
 CC DOMAIN 242 256  
 CC CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 257 277  
 CC POTENTIAL.  
 CC DOMAIN 278 301  
 CC EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 302 322  
 CC POTENTIAL.  
 CC DOMAIN 323 373  
 CC CYTOPLASMIC (POTENTIAL).  
 CC DISULFID 126 203  
 CC BY SIMILARITY.  
 CC SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;  
 Query Match 68.4%; Score 1346.5; DB 1; Length 373;  
 Best Local Similarity 76.9%; Pred. No. 1.1e-76;  
 Matches 257; Conservative 25; Mismatches 45; Indels 7; Gaps 3;  
 QY 1 MLSTSRFRIRNTNESGEVTTFFDYDGAPCHFDVKGQGAQLPPLSLVIFGFVGN 60  
 DB 14 ILTSHSLFPRSTQELDEGATPDYDGGEPCHKTSVKQIGAWILPPLSLVIFGFVGN 73  
 QY 61 MLVLLINCKKLCITDIYLLNLAISDLFLITPLMAHSAANEWVFGNCKLFTGLY 120  
 DB 74 MLVLLINCKKLCITDIYLLNLAISDLFLITPLMAHSAANEWVFGNCKLFTGLY 133  
 QY 121 HIGYFGGIFILLTIDRYLAIVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 DB 134 HIGYFGGIFILLTIDRYLAIVHAFVFAKARTVTFGVVTSVITWLVAVFASVPGIIFTK 193  
 QY 181 CQEDSVYVCGPYFPRGNWFFHTMRNLTGLVLLIMVICYSGILTKLLRCNEKKRHR 240  
 DB 194 SEQEDQHTCGPYFPTWKNFQIMRNILSLILPLVMVICYSGILTLFRCRNEKKRHR 253  
 QY 241 AVRFTIMIVYFLFWTPYVNIIVLLNTFQEFGLSNCESTSQDQATQVTTGLMTHCCI 300  
 DB 254 AVRFTIMIVYFLFWTPYVNIIVLLNTFQEFGLSNCESTSQDQATQVTTGLMTHCCI 313  
 QY 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327  
 DB 314 NPIIYAFVGEKFRRLSMF 347  
 RESULT 4  
 CKR2\_MOUSE STANDARD; PRT; 373 AA.  
 AC P51683; O61172;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-CR-2) (CCR-2) (CCR2)  
 DE (JE/FIC receptor) (MCP-1 receptor).  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



RA MEDLINE=98001387; PubMed=9343222;  
 RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 RT implicate specific amino acids in infections by simian and human  
 RT immunodeficiency viruses.";  
 RL J. Virol. 71:8642-8656(1997).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=97404635; PubMed=9261347;  
 RX Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,  
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;  
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human  
 RT immunodeficiency virus type 1";  
 RL J. Virol. 71:6305-6314(1997).  
 RP [6]  
 RP SEQUENCE FROM N.A.  
 RA Guo B., Kuno K., Hatada A., Matsushima K.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,  
 CC BUT NOT IN NONHEMATOPOIETIC CELL LINES.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 DR EMBL; U47036; AAC52454.1; -;  
 DR EMBL; X94151; CAA63867.1; -;  
 DR EMBL; U68565; AAB37273.1; -;  
 DR EMBL; U83327; AAC53386.1; -;  
 DR EMBL; AF022990; AAC53389.1; -;  
 DR EMBL; AF019772; AAB71183.1; -;  
 DR EMBL; D83648; BAA12024.1; -;  
 DR MGD; MGI:107182; Cmkbr5.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS; PR000237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.  
 FT DOMAIN 1 32  
 FT TRANSMEM 33 60  
 FT DOMAIN 61 70  
 FT TRANSMEM 71 91  
 FT DOMAIN 92 104  
 FT TRANSMEM 105 126  
 FT DOMAIN 127 143  
 FT TRANSMEM 144 168  
 FT DOMAIN 169 200  
 FT TRANSMEM 201 220  
 FT DOMAIN 221 237  
 FT TRANSMEM 238 262  
 FT DOMAIN 263 279  
 FT TRANSMEM 280 303  
 FT DOMAIN 304 334  
 FT DISULFID 103 180  
 FT CARBOHYD 270 270  
 FT VARIANT 11 11  
 FT VARIANT 62 62  
 FT VARIANT 66 66  
 FT VARIANT 97 97  
 FT VARIANT 109 109  
 FT VARIANT 156 156  
 FT VARIANT 160 160

FT VARIANT 185 185 P -> L.  
 FT VARIANT 213 213 I -> V.  
 FT VARIANT 318 318 I -> M.  
 FT VARIANT 337 337 V -> A.  
 FT CONFLICT 3 3 F -> L (IN REF. 2).  
 FT CONFLICT 80 80 L -> F (IN REF. 2).  
 FT CONFLICT 145 145 N -> I (IN REF. 5).  
 FT CONFLICT 190 190 H -> Y (IN REF. 3).  
 FT CONFLICT 208 208 P -> S (IN REF. 1).  
 SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;  
 Query Match 63.1%; Score 1244; DB 1; Length 354;  
 Best Local Similarity 75.3%; Pred. No. 2.2e-70;  
 Matches 232; Conservative 29; Mismatches 41; Indels 6; Gaps 2;  
 QY 17 GEEVTFDFDYDYG--APCHKFDVKQGAQLLPYLSLVFTGFVGNMVLVLLINCKKLLK 74  
 DB 5 GSVPTVIYDIDYDYGMSAPCKQKINVKQIAAQLLPYLSLVFTGFVGNMVLVLLINCKKLLK 64  
 QY 75 CLTDIYLLNLAISSDLLFLITPLWHAHSAANWVFGNAMCKLFTGLYHIGYFGGIFILL 134  
 DB 65 SVTDIYLLNLAISSDLLFLITPLWHAHSAANWVFGNAMCKLFTGLYHIGYFGGIFILL 124  
 QY 135 TIDRYLAIHVAHFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKQKEDSVVCGPYF 194  
 DB 125 TIDRYLAIHVAHFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKQKEDSVVCGPYF 184  
 QY 195 PRG----WNFTIMRNILGLVLPILIMVTCYSGILKTLRCRNEKRRHRAVRVIFTIMI 250  
 DB 185 PHQYHFWKSFQTLKVMVLSLILPLLVMIITCYSGILHTRFCRNEKRRHRAVRVIFTIMI 244  
 QY 251 VYLFWTPXNIVILLNTFQEFFGLSNCESTSQLDQATQVETGLTGMTHCCINPIYAFVGE 310  
 DB 245 VYLFWTPXNIVILLNTFQEFFGLSNCESTSQLDQATQVETGLTGMTHCCINPIYAFVGE 304  
 QY 311 KFRSLFHI 318  
 DB 305 KFRSLSV 312  
 RESULT 6  
 CKR5\_CERTO STANDARD; PRT; 352 AA.  
 ID CKR5\_CERTO 062743; 062744; 062745; 062746;  
 AC 062743; 062744; 062745; 062746;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-CR-5) (CC-CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKBR5.  
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OC NCBI\_TaxID=9531;  
 OX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Isolate 079, 085, 087, and 089;  
 RX MEDLINE=98321155; PubMed=9656999;  
 RA Chen Z., Gettie A., Ho D.D., Marx P.A.;  
 RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys  
 RT naturally infected in west Africa: a comparison of coreceptor usage  
 RT of primary SIVsm, HIV-2, and SIVmac.";  
 RL Virology 246:113-124(1998).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 CC DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC







QY 258 PYNIVILLNTFQEFGLSNCSTESQLOQAVTETLGTHTCCINPIIYAFVGEKFRSLF- 316  
 Db 250 PYNIVILLNTFQEFGLSNCSTESQLOQAVTETLGTHTCCINPIIYAFVGEKFRSLF- 309  
 QY 317 -----HIA 319  
 Db 310 VFFQKHIA 317

RESULT 9  
 CKR5\_PANTR STANDARD; PRT; 352 AA.  
 AC P56440; 002778;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CKR5 OR CMKBR5.  
 OS Pan troglodytes (Chimpanzee).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.  
 NCBI\_TaxID=9598;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CKR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Zimmerman P.A., Buckler-White A., Alkhatib G.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=98022612; PubMed=9359654;  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang B.,  
 RA Ho D.D.;  
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";  
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=97426118; PubMed=9282822;  
 RA Zacharova V., Zachar V., Goustin A.S.;  
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural  
 RT HIV type 1 host";  
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=98090115; PubMed=9430250;  
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;  
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1";  
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 CC DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; AF005663; AAB62557.1; -;  
 DR EMBL; U94329; AAB58446.1; -;

DR EMBL; AF011542; AAB65742.1; -;  
 DR EMBL; U97666; AAC51670.1; -;  
 DR EMBL; AF011540; AAB65740.1; -;  
 DR EMBL; U89797; AAC03717.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCR\_Rhodopsn.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30  
 FT TRANSMEM 31 58  
 FT DOMAIN 59 68  
 FT TRANSMEM 69 89  
 FT DOMAIN 90 102  
 FT TRANSMEM 103 124  
 FT DOMAIN 125 141  
 FT TRANSMEM 142 166  
 FT DOMAIN 167 198  
 FT TRANSMEM 199 218  
 FT DOMAIN 219 235  
 FT TRANSMEM 236 260  
 FT DOMAIN 261 277  
 FT TRANSMEM 278 301  
 FT DOMAIN 302 352  
 FT DISULFID 101 178  
 FT MOD\_RES 3 3  
 FT MOD\_RES 10 10  
 FT MOD\_RES 14 14  
 FT MOD\_RES 15 15  
 FT CARBOHYD 268 268  
 FT CONFLICT 123 123  
 SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;  
 Query Match 62.4%; Score 1230; DB 1; Length 352;  
 Best Local Similarity 76.9%; Pred. No. 1.6e-69;  
 Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;  
 QY 24 FDYD--CAPCHKFDVKQIGALLPPLYSILVFFGVGNMVLVLLINCKKLCITDIYL 81  
 Db YDIIDYTTSEPCQKINVKQIAARLLPPLYSILVFFGVGNMVLVLLINCKKLSMTDIYL 69  
 QY 82 LNLAISDLLFLITPLWHAASAANEVFGNAMCKLFTGLYHIGYFGGIFITLITIDRYLA 141  
 Db LNLAISDLLFFLTVPFWAHYAAQWDFGNTMQLLTGLYFGFGIFITLITIDRYLA 129  
 QY 142 IVHAVFALKARTVTGVVTSVITWLVAVFASVPGIITFCOKEDSVVCGPVP---RG 197  
 Db IVHAVFALKARTVTGVVTSVITWLVAVFASVPGIITFCOKEDSVVCGPVP---RG 197  
 QY 198 WNNFHTIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHRVAVFTIMIVYFLFWT 257  
 Db WNNFHTIMRNILGLVLPPLIMVICYSGILKTLRCRNEKKRHRVAVFTIMIVYFLFWT 249  
 QY 258 PYNIVILLNTFQEFGLSNCSTESQLOQAVTETLGTHTCCINPIIYAFVGEKFRSLF- 316  
 Db PYNIVILLNTFQEFGLSNCSTESQLOQAVTETLGTHTCCINPIIYAFVGEKFRSLF- 309  
 QY 317 -----HIA 319  
 Db 310 VFFQKHIA 317

RESULT 10  
 CKR5\_PONPY STANDARD; PRT; 352 AA.  
 ID CKR5\_PONPY  
 AC O97881;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).  
 GN CKR5 OR CMKBR5.  
 OS Pongo pygmaeus (Orangutan).



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.  
 OX NCBI\_TaxID=9600;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99416438; PubMed=10486970;  
 RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
 RT "Sequence evolution of the CKR5 chemokine receptor gene in primates."  
 RL Mol. Biol. Evol. 16:1145-1154(1999).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 CC DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; AF075446; AAD19858.1;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 4 (POTENTIAL).  
 FT TRANSMEM 142 166 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 167 198 5 (POTENTIAL).  
 FT TRANSMEM 199 218 6 (POTENTIAL).  
 FT DOMAIN 219 235 7 (POTENTIAL).  
 FT TRANSMEM 236 260 8 (POTENTIAL).  
 FT DOMAIN 261 277 9 (POTENTIAL).  
 FT TRANSMEM 278 301 10 (POTENTIAL).  
 FT DOMAIN 302 332 11 (POTENTIAL).  
 FT TRANSMEM 333 352 12 (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 352 AA; 40527 MW; F4E2F47135AF658A CRC64;  
 SQ SEQUENCE 352 AA; 62.4%; Score 1230; DB 1; Length 352;  
 Query Match Best Local Similarity 76.9%; Pred. No. 1.6e-69;  
 Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;  
 QY 24 FDYD--GAPCHFDVKQIAQLLPPLYSLVFIFGFGNMLVLLINCKKLCITDIYL 81  
 DB 10 YDIYTTSEPCQKINVKYIAARLLPPLYSLVFIFGFGNMLVLLINCKKLSMTDIYL 69  
 QY 82 LNLASDLFLIITLPWAHSAANEWFGNACMLFTGLYHIGYFGGFIITLITIDRYLA 141  
 DB 70 LNLASDLFLIITLPWAHSAANEWFGNACMLFTGLYHIGYFGGFIITLITIDRYLA 129  
 QY 142 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYEP----RG 197  
 DB 130 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYEP----RG 189  
 QY 198 WNNFHTMRLNLGLVLPDLLMVICYSIGILKTLRCRKRHRRAVRVIFIMIVYFLWT 257  
 DB 190 WKNFQTLKIVLGLVLPDLLMVICYSIGILKTLRCRKRHRRAVRVIFIMIVYFLWA 249

QY 258 PYNIVILLNTFOEFFGLSNCESTSDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLP- 316  
 DB 250 PYNIVILLNTFOEFFGLSNCESTSDQATQVTEITLGMTHCCINPIIYAFVGEKFRNYLL 309  
 QY 317 -----HIA 319  
 DB 310 VFFQKHIA 317  
 RESULT 11  
 ID CKR5\_RAT STANDARD; PRT; 354 AA.  
 AC O08556;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DE 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (MIP-1  
 DE alpha receptor).  
 GN CCR5 OR CNKR5.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Wistar; TISSUE=Brain;  
 RX MEDLINE=98334064; PubMed=9670989;  
 RA Speleiss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,  
 RA Berger M., Gebicke-Haerter P.J.;  
 RT "Cloning of rat HIV-1-chemokine coreceptor CCR5 from microglia and  
 RT upregulation of its mRNA in ischemic and endotoxinemic rat brain."  
 RL J. Neurosci. Res. 53:16-28(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=Sprague-Dawley;  
 RX MEDLINE=98318173; PubMed=9655467;  
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 RT "Chemokine receptor expression in cultured glia and rat experimental  
 RT allergic encephalomyelitis."  
 RL J. Neuroimmunol. 86:1-12(1998).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; Y12009; CAA72737.1;  
 DR EMBL; U77350; AAC03243.1;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 33 60 1 (POTENTIAL).  
 FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 71 91 2 (POTENTIAL).  
 FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 105 126 3 (POTENTIAL).  
 FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 144 168 4 (POTENTIAL).  
 FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).

TRANSMEM 201 220 5 (POTENTIAL).  
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 238 262 6 (POTENTIAL).  
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 280 303 7 (POTENTIAL).  
 FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 103 180 BY SIMILARITY.  
 FT CARBOHYD 270 270 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 62.4%; Score 1230; DB 1; Length 354;  
 Best Local Similarity 75.0%; Pred. No. 1.6e-69;  
 Matches 231; Conservative 29; Mismatches 42; Indels 6; Gaps 2;

QY 17 GEEVTFEDYD--GAPCHKEDVQIGQALLPPLYSLVFIQFVGNMVLVILINCKKLK 74  
 Db 5 GSIPYIYIDISAPCQVNNVQIAAQLPPLYSLVFIQFVGNMVLVILINCKKLK 64  
 QY 75 CLTDIYLLNLAISDLLFLITLPLWAHSAANEVFNAMCKLFTGLYHIGYGGIIFILL 134  
 65 SMTDIYLFNLAISDLLFLITLPLWAHSAANEVFNAMCKLFTGLYHIGYGGIIFILL 124  
 QY 135 TIDRYLAIVAFALKARTVTFGVVTSVITWLVAFASVPGIIFTCOKEDSVYVCGPYF 194  
 125 TIDRYLAIVAFALKARTVTFGVVTSVITWLVAFASVPGIIFTCOKEDSVYVCGPYF 184  
 QY 195 ----PRGWNPHITMRNLGLVPLLLIMVICYSGILKTLRCRNEKKRHRAVRVFTMI 250  
 185 LHQYREKHFQILKWILSLLPLVWVICYSGILNTLFCRNEKKRHRAVRVFTMI 244  
 QY 251 VYLFPTPNVILNLTQFEGFGLSNCSTSQLDQATQVETLGTHTCCINPIYAFVGE 310  
 245 VYLFPTPNVILNLTQFEGFGLSNCSTSQLDQATQVETLGTHTCCINPIYAFVGE 304  
 QY 311 KFRSLPHI 318  
 305 KFRNLSV 312

RESULT 12  
 ID CKR5 GORGO STANDARD; PRT; 352 AA.  
 AC P56439;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CR-5) (CCR-5) (CCR5).  
 GN CKR5 OR CMKBR5  
 GN Gorilla gorilla gorilla (Lowland gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 RN NCBI\_TaxID=9595;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains".  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 CC DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 or send an email to license@isb-sib.ch).

EMBL; AF005659; AAB62553.1;  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR Pfam; PF00001; 7tm.1.1;  
 DR PRINTS; PR00237; GPCR\_Rhodopsin  
 DR PROSITE; PS00237; G-PROTEIN\_RECP\_F1\_1;  
 DR PROSITE; PS00237; G-PROTEIN\_RECP\_F1\_2;  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 62.3%; Score 1228; DB 1; Length 352;  
 Best Local Similarity 76.9%; Pred. No. 2.1e-69;  
 Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYD--GAPCHKEDVQIGQALLPPLYSLVFIQFVGNMVLVILINCKKLKLTIDYL 81  
 Db 10 YDIYDTSEPCQKTNVQIAARLLPPLYSLVFIQFVGNMVLVILINCKKLKSMTDYL 69  
 QY 82 LNLASDLLFLITLPLWAHSAANEVFNAMCKLFTGLYHIGYGGIIFILLTIDRYLA 141  
 70 LNLASDLLFLITLPLWAHSAANEVFNAMCKLFTGLYHIGYGGIIFILLTIDRYLA 129  
 QY 142 IVHAVFALKARTVTFGVVTSVITWLVAFASVPGIIFTCOKEDSVYVCGPYF 197  
 130 IVHAVFALKARTVTFGVVTSVITWLVAFASVPGIIFTCOKEDSVYVCGPYF 189  
 QY 198 WNNFHTMRNLGLVPLLLIMVICYSGILKTLRCRNEKKRHRAVRVFTMIYVFLFW 257  
 190 WNFQTKLTVLGLVPLLLIMVICYSGILKTLRCRNEKKRHRAVRVFTMIYVFLFW 249  
 QY 258 PYNIVLLNTQFEGFGLSNCSTSQLDQATQVETLGTHTCCINPIYAFVGEKFRSLF 316  
 250 PYNIVLLNTQFEGFGLSNCSTSQLDQATQVETLGTHTCCINPIYAFVGEKFRSLF 309  
 QY 317 -----HIA 319  
 310 VFFQKHIA 317

## RESULT 13

CKR5\_PAPHA STANDARD; PRT; 352 AA.  
 ID CKR5\_PAPHA  
 AC P56441;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CR-5) (CCR-5) (CCR5).  
 GN CKR5 OR CMKBR5.  
 GN Papio hamadryas (Hamadryas baboon), and  
 OS Papio anubis (Olive baboon).





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FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION.
FT MOD_RES 10 10 SULFATION.
FT MOD_RES 14 14 SULFATION.
FT MOD_RES 15 15 SULFATION.
FT VARIANT 10 10 Y -> D (IN INCCR5-71A).
FT VARIANT 29 29 /FTIQ=VAR_003481.
FT VARIANT 31 31 A -> S (IN DBSNP:1800939).
FT VARIANT 31 31 /FTIQ=VAR_011839.
FT VARIANT 31 31 R -> H (IN INCCR5-72A).

Query Match 62.1%; Score 1224; DB 1; Length 352;
Best Local Similarity 76.3%; Pred. No. 3.8e-69;
Matches 235; Conservative 27; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYDY--GAPCHKFDVKQIAQLLPPLYSLVFIFGVGNMVLVILINCKKLCITDIYL 81
Db 10 YDINYTSEPCQKINVKQIAARLLPPLYSLVFIFGVGNMVLVILINCKKLCITDIYL 69
QY 82 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFILLITDIYLA 141
Db 70 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFILLITDIYLA 129
QY 142 IVHAVFALKARTVTFGVVTSVITLWLVAVFASVPGIIFTKCKEDSVVCGPYFP--RG 197
Db 130 VHAVFALKARTVTFGVVTSVITLWLVAVFASVPGIIFTRSQEGLHYTCSSHPYSQYQF 189
QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVIETIMIVFLFWT 257
Db 190 WKNFQTLKIVLGLVPLLMVICYSGILKTLRCRNEKKRHRVAVIETIMIVFLFWA 249
QY 258 PYNIVILLNTFOEFFGLSNCESTSOLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 316
Db 250 PYNIVILLNTFOEFFGLSNCESTSOLDQATQVTEITLGMTHCCINPIIYAFVGEKFRNLL 309
QY 317 -----HIA 319
Db 310 VFFQKHIA 317

RESULT 15
CKR5_PYGNE
ID CKR5_PYGNE STANDARD; PRT; 352 AA.
AC OS7862;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5).
GN CKR5 OR CMKBR5.
OS Pygathrix nemaeus (Dove langur).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OC NCBI_TaxID=54133;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99416438; PubMed=10486970;
RT Zhang Y.-W., Ryder O.A., Zhang Y.-P.;
RA "Sequence evolution of the CCR5 chemokine receptor gene in primates.";
RL Mol. Biol. Evol. 16:1145-1154(1999).
CC -1- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR
CC DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

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CC CC -----
CC CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC CC -----
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CC CC -----
CC CC EMBL: AF075448; AAD19860.1; -
CC CC InterPro: IPR000276; GPCR_Rhodpsn.
CC CC Pfam: PF00001; 7tm.1; 1.
CC CC PRINTS: PRO0237; GPCR_Rhodopsin.
CC CC PROSITE: PS00237; G-PROTEIN_RECP_FL_1; 1.
CC CC PROSITE: PS00262; G-PROTEIN_RECP_FL_2; 1.
CC CC G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
KW DOMAIN 1 30 EXTRACELLULAR (POTENTIAL)..
FT TRANSMEM 31 58 1 (POTENTIAL).
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 69 89 2 (POTENTIAL).
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 124 3 (POTENTIAL).
FT DOMAIN 125 141 4 (POTENTIAL).
FT TRANSMEM 142 166 4 (POTENTIAL).
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 199 218 5 (POTENTIAL).
FT DOMAIN 219 235 5 (POTENTIAL).
FT TRANSMEM 236 260 6 (POTENTIAL).
FT DOMAIN 261 277 7 (POTENTIAL).
FT TRANSMEM 278 301 7 (POTENTIAL).
FT DOMAIN 302 352 7 (POTENTIAL).
FT DISULFID 101 178 BY SIMILARITY.
FT MOD_RES 3 3 SULFATION (BY SIMILARITY).
FT MOD_RES 10 10 SULFATION (BY SIMILARITY).
FT MOD_RES 14 14 SULFATION (BY SIMILARITY).
FT MOD_RES 15 15 SULFATION (BY SIMILARITY).
SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E861 CRC64;

Query Match 62.1%; Score 1224; DB 1; Length 352;
Best Local Similarity 76.9%; Pred. No. 3.8e-69;
Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYDY--GAPCHKFDVKQIAQLLPPLYSLVFIFGVGNMVLVILINCKKLCITDIYL 81
Db 10 YDINYTSEPCQKINVKQIAARLLPPLYSLVFIFGVGNMVLVILINCKKLCITDIYL 69
QY 82 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFILLITDIYLA 141
Db 70 LNLAISDLLFLITLPLWAHSAANEVFGNAMCKLFTGLYHIGYFGGIFILLITDIYLA 129
QY 142 IVHAVFALKARTVTFGVVTSVITLWLVAVFASVPGIIFTKCKEDSVVCGPYFP--RG 197
Db 130 IVHAVFALKARTVTFGVVTSVITLWLVAVFASVPGIIFTRSQEGLHYTCSSHPYSQYQF 189
QY 198 WNNFHTIMRNILGLVPLLMVICYSGILKTLRCRNEKKRHRVAVIETIMIVFLFWT 257
Db 190 WKNFQTLKIVLGLVPLLMVICYSGILKTLRCRNEKKRHRVAVIETIMIVFLFWA 249
QY 258 PYNIVILLNTFOEFFGLSNCESTSOLDQATQVTEITLGMTHCCINPIIYAFVGEKFRSLF- 316
Db 250 PYNIVILLNTFOEFFGLSNCESTSOLDQATQVTEITLGMTHCCINPIIYAFVGEKFRNLL 309
QY 317 -----HIA 319
Db 310 VFFQKHIA 317

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Job time : 16.7956 secs

